WHAT IS CLAIMED IS:

1. A substantially purified polypeptide comprising:

(a) 16-36 amino acids in length; and

(b) comprising the sequence NH_2-$X_1X_2X_3X_4X_5X_6$IKKX_7F$X_8X_9X_{10}$LX_{11}P-COOH (SEQ ID NO:1), wherein X_1, X_2, and X_6 are individually K or R; wherein X_3 is I or K; wherein X_4 is V or G; wherein X_5 is Q or R; wherein X_7, X_9, X_{10}, and X_{11} are each individually any amino acid; wherein X_8 is L or F and wherein the polypeptide comprises antimicrobial, antifungal, and/or antiviral activity.

2. The substantially purified polypeptide of claim 1, wherein the polypeptide is about 16 to 20 amino acids in length.

3. The substantially purified polypeptide of claim 2, wherein the polypeptide comprises a sequence selected from the sequence consisting of:

(a) NH_2-KRIVQRIKDFLRNLVP-COOH (SEQ ID NO:13);

(b) NH_2-KRIVQRIKDFLRNLVPR-COOH (SEQ ID NO:14);

(c) NH_2-KRIVQRIKDFLRNLVPRT-COOH (SEQ ID NO:15);

(d) NH_2-KRIVQRIKDFLRNLVPRTE-COOH (SEQ ID NO:16); and

(e) NH_2-KRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:17).

4. The substantially purified polypeptide of claim 1, wherein the polypeptide is about 26 to 30 amino acids in length.

5. The substantially purified polypeptide of claim 4, wherein the polypeptide comprises a sequence selected from the group consisting of:

(a) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVP-COOH (SEQ ID NO:18);

(b) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPR-COOH (SEQ ID NO:19);

(c) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPRT-COOH (SEQ ID NO:20);

(d) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPRTE-COOH (SEQ ID NO:21); and

(e) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:22).

6. The substantially purified polypeptide of claim 1, wherein the polypeptide is about 27 to 31 amino acids in length.

7. The substantially purified polypeptide of claim 6, wherein the polypeptide comprises a sequence selected from the group consisting of:

(a) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVP-COOH (SEQ ID NO:23);

(b) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPR-COOH (SEQ ID NO:24);

(c) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPRT-COOH (SEQ ID NO:25);

(d) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPRTE-COOH (SEQ ID NO:26);

(e) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:27).

8. The substantially purified polypeptide of claim 1, wherein the polypeptide is 36 amino acids in length.

9. The substantially purified polypeptide of claim 8, wherein the polypeptide consists of the sequence NH_2-LGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:28).

10. An isolated polynucleotide encoding the polypeptide of any one of claims 1-9.

11. An isolated polynucleotide comprising 45 to 108 nucleotides in length and encoding a cathelicidin function fragment, wherein the polynucleotide comprises a sequence selected from the group consisting of:

(a) a sequence encoding NH_2-$X_1X_2X_3X_4X_5X_6$IKX$_7$F$X_8X_9X_{10}$LX_{11}P-COOH (SEQ ID NO:1), wherein X_1, X_2, and X_6 are individually K or R; wherein X_3 is I or K; wherein X_4 is V or G; wherein X_5 is Q or R; wherein X_7, X_9, X_{10}, and X_{11} are each individually any amino acid; wherein X_8 is L or F and wherein the polypeptide comprises antimicrobial and/or antiviral activity;

(b) a sequence encoding NH_2-KRIVQRIKDFLRNLVPRTES- COOH (SEQ ID NO:17);

(c) a sequence encoding NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:22);

(d) a sequence encoding NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:27);

(e) a sequence encoding NH_2-LGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:28);

(f) a fragment of (b)-(e) that encodes a polypeptide containing SEQ ID NO:1 and is at least 16 amino acids in length;

(g) SEQ ID NO:5 from about nucleotide 451 to 498, from about nucleotide 451 to 501, from about nucleotide 451 to 504, from about nucleotide 451 to 507, from about nucleotide 451 to 510, from about nucleotide 421 to 498, from about nucleotide 421 to 501, from about nucleotide 421 to 504, from about nucleotide 421 to 507, from about nucleotide 421 to 510, from about nucleotide 418 to 498, from about nucleotide 418 to 501, from about nucleotide 418 to 504, from about nucleotide 418 to 507, from about nucleotide 418 to 510, from about nucleotide 403 to 498, from about nucleotide 403 to 501, from about nucleotide 403 to 504, from about nucleotide 403 to 507, or from about nucleotide 403 to 510;

(h) the sequence of (g) wherein T can be U; and

(i) the sequence complementary to the sequence of (g) or (h).

12. A vector comprising the polynucleotide of claim 10.

13. A vector comprising the polynucleotide of claim 11.

14. A recombinant host cell comprising the polynucleotide of claim 10.

15. A recombinant host cell comprising the polynucleotide of claim 11.

16. A recombinant host cell comprising the vector of claim 12.

17. A recombinant host cell comprising the vector of claim 13.

18. A method of producing a cathelicidin functional fragment comprising culturing the host cell of any one of claim 14-17 under conditions in which the host cell produces the cathelicidin functional fragment and substantially purifying the cathelicidin functional fragment.

19. A method of inhibiting the growth of a microbe comprising contacting the microbe with an inhibiting effective amount of a peptide that is 16-36 amino acids in length; and contains the sequence NH_2-$X_1X_2X_3X_4X_5X_6$IKX$_7$F$X_8X_9X_{10}$LX_{11}P-COOH (SEQ ID NO:1), wherein X_1, X_2, and X_6 are individually K or R; wherein X_3 is I or K; wherein X_4 is V or G; wherein X_5 is Q or R; wherein X_7, X_9, X_{10}, and X_{11} are each individually any amino acid; wherein X_8 is L or F and wherein the polypeptide comprises antimicrobial, antifungal, and/or antiviral activity.

20. The method of claim 19, wherein the peptide is about 16 to 20 amino acids in length.

21. The method of claim 20, wherein the peptide comprises a sequence selected from the group consisting of:

(a) NH_2-KRIVQRIKDFLRNLVP-COOH (SEQ ID NO:13);

(b) NH_2-KRIVQRIKDFLRNLVPR-COOH (SEQ ID NO:14);

(c) NH_2-KRIVQRIKDFLRNLVPRT-COOH (SEQ ID NO:15);

(d) NH_2-KRIVQRIKDFLRNLVPRTE-COOH (SEQ ID NO:16); and

(e) NH_2-KRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:17).

22. The method of claim 19, wherein the polypeptide is about 26 to 30 amino acids in length.

23. The method of claim 22, wherein the peptide comprises a sequence selected from the group consisting of:

(a) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVP-COOH (SEQ ID NO:18);

(b) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPR-COOH (SEQ ID NO:19);

(c) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPRT-COOH (SEQ ID NO:20);

(d) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPRTE-COOH (SEQ ID NO:21); and

(e) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:22).

24. The method of claim 19, wherein the peptide is about 27 to 31 amino acids in length.

25. The method of claim 24, wherein the peptide comprises a sequence selected from the group consisting of:

(a) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVP-COOH (SEQ ID NO:23);

(b) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPR-COOH (SEQ ID NO:24);

(c) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPRT-COOH (SEQ ID NO:25);

(d) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPRTE-COOH (SEQ ID NO:26);

(e) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:27).

26. The method of claim 19, wherein the peptide is 36 amino acids in length.

27. The method of claim 26, wherein the peptide consists of the sequence NH_2-LGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:28).

28. The method of claim 19, wherein the contacting is *in vitro*.

29. The method of claim 28, wherein the contacting is on a surface suspected of having a microbe.

30. The method of claim 29, wherein the microbe is selected from the group consisting of a virus or viral particle, a bacteria, and a fungal organism.

31. The method of claim 19, wherein the contacting is *in vivo*.

32. The method of claim 31, wherein the contacting *in vivo* is by topical administration.

33. The method of claim 30, wherein the bacteria is gram positive.

34. The method of claim 33, wherein bacteria is *Staphylococcus aureus* or *S. epidermidis*.

35. The method of claim 30, wherein the bacteria is gram negative.

36. The method of claim 35, wherein the bacteria is selected from the group consisting of *E. coli*, *P. aeruginosa*, and *S. typhimurium*.

37. The method of claim 19, wherein the peptide is administered in combination with at least one antibiotic.

38. The method of claim 37, wherein the class of antibiotic is selected from the group consisting of aminoglycosides, penicillins, cephalosporins, carbapenems, monobactams, quinolones, tetracyclines, glycopeptides, chloramphenicol,

clindamycin, trimethoprim, sulfamethoxazole, nitrofuirantoin, rifampin and mupirocin.

39. The method of claim 37, wherein the antibiotic is selected from the group consisting of amikacin, gentamicin, kanamycin, netilmicin, t-obramycin, streptomycin, azithromycin, clarithromycin, erythromycin, erythromycin estolate/ethylsuccinate/gluceptatellactobionate/stearate, penicillin G, penicillin V, methicillin, nafcillin, oxacillin, cloxacillin, dicloxacillin, ampicillin, amoxicillin, ticarcillin, carbenicillin, mezlocillin, azlocillin, piperacillin, cephalothin, cefazolin, cefaclor, cefamandole, cefoxitin, cefuiroxime, cefonicid, cefmetazole, cefotetan, cefprozil, loracarbef, cefetamet, cefoperazone, cefotaxime, ceftizoxime, ceftriaxone, ceftazidime, cefepime, cefixime, cefpodoxime, cefsulodin, i-mipenem, aztreonam, fleroxacin, nalidixic acid, norfloxacin, ciprofloxacin, ofloxacin, enoxacin, lomefloxacin, cinoxacin, doxycycline, m-inocycline, tetracycline, vancomycin, and teicoplanin.

40. A composition comprising a cathelicidin functional fragment of any one of claim 1-9 and a pharmaceutically acceptable carrier.

41. The composition of claim 40, wherein the composition is a lotion, cream, gel, ointment or spray.

42. The pharmaceutical composition of claim 40, wherein the pharmaceutical compositions is for topical administration.

43. The pharmaceutical composition of claim 40, comprising a carbonate buffer system.

44. The pharmaceutical composition of claim 43, wherein the carbonate buffer system comprises a bicarbonate concentration of between about 15 mM and about 500 mM bicarbonate.

45. A method of stimulating LL-37 activity or a cathelicidin functional fragment activity in a sample, comprising

contacting the sample with an effective amount of a carbonate composition.

46. A method of stimulating LL-37 activity or a cathelicidin functional fragment activity in a subject, comprising

contacting the subject with an effective amount of a carbonate composition.

47. The method of claim 42 or 43, wherein the carbonate composition comprises a bicarbonate.

48. The method of claim 47, wherein the bicarbonate comprises between about 15 mM and about 500 mM bicarbonate.

49. A method of generating a cathelicidin functional fragment comprising contacting a substantially purified LL-37 with a protease under condition to generate a cathelicidin functional fragment comprising SEQ ID NO:17, SEQ ID NO:22, and/or SEQ ID NO:27.

50. A method of decontaminating a surface comprising contacting the surface with a composition comprising a cathelicidin functional fragment.

51. The method of claim 50, wherein the composition comprises a carbonate buffer.

52. The method of claim 51, wherein the carbonate buffer comprises bicarbonate.

53. The method of claim 52, wherein the bicarbonate comprises between about 15 mM and 500 mM bicarbonate.

54. The method of claim 50, wherein the composition is in the form of a lotion, cream, gel, ointment or spray.

55. The method of claim 50, wherein the cathelicidin functional fragment comprises a peptide having a sequence NH_2-$X_1X_2X_3X_4X_5X_6IKX_7FX_8X_9X_{10}LX_{11}P$-COOH (SEQ ID NO:1), wherein X_1, X_2, and X_6 are individually K or R; wherein X_3 is I or K; wherein X_4 is V or G; wherein X_5 is Q or R; wherein X_7, X_9, X_{10}, and X_{11} are each individually any amino acid; wherein X_8 is L or F and wherein the polypeptide comprises antimicrobial, antifungal, and/or antiviral activity.

56. The method of claim 55, wherein the polypeptide is about 16 to 20 amino acids in length.

57. The method of claim 56, wherein the polypeptide comprises a sequence selected from the sequence consisting of:

(a) NH_2-KRIVQRIKDFLRNLVP-COOH (SEQ ID NO:13);

(b) NH_2-KRIVQRIKDFLRNLVPR-COOH (SEQ ID NO:14);

(c) NH_2-KRIVQRIKDFLRNLVPRT-COOH (SEQ ID NO:15);

(d) NH_2-KRIVQRIKDFLRNLVPRTE-COOH (SEQ ID NO:16); and

(e) NH_2-KRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:17).

58. The method of claim 55, wherein the polypeptide is about 26 to 30 amino acids in length.

59. The method of claim 58, wherein the polypeptide comprises a sequence selected from the group consisting of:

(a) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVP-COOH (SEQ ID NO:18);

(b) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPR-COOH (SEQ ID NO:19);

(c) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPRT-COOH (SEQ ID NO:20);

(d) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPRTE-COOH (SEQ ID NO:21); and

(e) NH_2-KSKEKIGKEFKRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:22).

60. The method of claim 55, wherein the polypeptide is about 27 to 31 amino acids in length.

61. The method of claim 60, wherein the polypeptide comprises a sequence selected from the group consisting of:

(a) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVP-COOH (SEQ ID NO:23);

(b) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPR-COOH (SEQ ID NO:24);

(c) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPRT-COOH (SEQ ID NO:25);

(d) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPRTE-COOH (SEQ ID NO:26);

(e) NH_2-RKSKEKIGKEFKRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:27).

62. The method of claim 55, wherein the polypeptide is 36 amino acids in length.

63. The method of claim 62, wherein the polypeptide consists of the sequence NH_2-LGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES-COOH (SEQ ID NO:28).

64. A method of stimulating inflammation comprising contacting an epithelial cell with an LL-37 derived peptide.

65. The method of claim 64, wherein the epithelial cell is a keratinocyte.

66. The method of claim 64, wherein the peptide simulates the release of pro-inflammatory mediators form the epithelial cell.

67. A method of inhibiting the release of pro-inflammatory mediators from dendritic cells comprising contacting the cell with an LL-37 derived peptide.

68. The method of claim 19, wherein the microbe is associated with atopic dermatitis.